REMARKS

Restriction Requirement:

Claims 21-25 and 27-56, directed to non-elected inventions, have been canceled without prejudice to or disclaimer of the subject matter therein. Applicants expressly reserve the right to pursue the subject matter of the non-elected claims in divisional applications without the need to file a terminal disclaimer.

Claim Amendments:

Claim 1 has been amended to add functional language. Support for this amendment and all similar amendments in other claims is found in the specification on pages 43-47, and in Examples 3, 4, 5, 18-21 and 27.

All claims have been amended to recite an "isolated" protein. Support for the amendment is found in the specification on page 5, lines 3-5.

Support for the reference to retention of "biological activity" of fragments and variants is found on page 4, lines 11-13 and lines 25-26.

Support for the amendment to Claim 19 is found in the specification on page 5, line 29 to page 6, line 16.

Support for added Claims 57-61 is found in the specification on page 3, lines 1-5; page 4, lines 25-26; pages 43-47, and in the Examples.

Support for added Claims 62 and 63 is found on page 6, lines 29-30.

Support for added Claim 64 is found on pages 43-47 and Examples 3, 4, 5, 18-21 and 27.

Support for added Claim 65 is found on pages 43-47 and Examples 3, 4, 5, 18-21 and 27.

Objection to the Disclosure:

The Examiner has objected to the disclosure, requiring that the sequence identification numbers used the format provided in 37 CFR § 1.821 (SEQ ID NO:). The specification and claims have been amended throughout to use the format as required by the Examiner.

The Examiner has also required that the priority applications be cross-referenced at page 1. The specification has been amended to insert the priority claim.

The disclosure is also objected to because of the use of an embedded hyperlink. The specification has been amended to delete the embedded hyperlinks and to insert therefore the actual citations of references as provided on the originally referenced website, which was incorporated by reference. Also enclosed is the requisite Declaration by the below-named agent which states that the amendatory material consists of the same material incorporated by reference into the specification.

Drawings

The Examiner has stated that formal drawings may be submitted when the application is allowed. Applicants will submit formal drawings as required by the Examiner upon allowance of the application.

Objection to the Claims:

The Examiner has objected to Claim 3 as being a substantial duplicate of Claim 2. Claim 3 has been canceled without prejudice to or disclaimer of the subject matter therein.

Rejection of Claims 1-18, 20 and 26 Under 35 U.S.C. § 101:

The Examiner has rejected Claims 1-18, 20 and 26 under 35 U.S.C. § 101, contending that these claims are directed to non-statutory subject matter, since the claims do not recite an "isolated" or "purified" protein.

Claims 1-18, 20 and 26 have been amended to insert the term "isolated" prior to the term "protein," thereby indicating statutory subject matter. The Examiner is respectfully requested to withdraw the rejection of Claims 1-18, 20 and 26 under 35 U.S.C. § 101.

Objection to the Specification and Rejection of Claims 1-3, 13-17 18, 20 and 26 Under 35 U.S.C. § 112, First Paragraph:

The Examiner has objected to the specification and rejected Claims 1-3, 13-17 18, 20 and 26 under 35 U.S.C. § 112, first, paragraph, on the basis of enablement. Specifically, the Examiner acknowledges that the specification enables proteins capable of affecting ABA response and

comprising the hydrophobic C-terminal, coiled coil region, EF- and consensus sequence, nucleotide binding site, hydrophobic N-terminal of SEQ ID NO:2, the Abl1 gene product having calcium-modulated protein phosphatase comprising an EF hand consensus sequence, and the DS2 protein having a hydrophilic N-terminal, a coiled-coil region and a hydrophobic C-terminal. However, the Examiner contends that the specification does not enable all proteins comprising these features and variants thereof. The Examiner asserts that over 150 genes have been shown to be responsive to ABA and that the multitudes of encoded proteins that would be considered to affect ABA signaling are not disclosed by sequence structure. Furthermore, the Examiner contends that the function of the proteins are not set forth in the specification and therefore identification of the protein via its function in growth and development or during stress and its function in the ABA response is not disclosed. Therefore, the Examiner concludes that identification of proteins meeting the claim limitations would require undue experimentation.

Applicants respectfully traverse the Examiner's rejection of Claims 1-3, 13-17, 18, 20 and 26 under 35 U.S.C. § 112, first paragraph.

Initially, Applicants note that Claim 1 has been amended to recite that the protein comprises four and optionally, five, of the recited structural features, as well as a specific function of the protein with regard to ABA signaling that has been identified in the present specification. More particularly, Claim 1 now recites that the claimed protein affects ABA signalling as measured by its ability to affect ABA-mediated control of ion channels. This is a specific biological function of the proteins of the present invention, and assays describing how to measure this activity are described in great detail in the specification (see, for example, pages 43-47, and Examples 3, 4, 5, 18-21 and 27). Contrary to the Examiner's contention that the function of the proteins are not set forth in the specification, Applicants submit that the function of the proteins in the ABA response is set forth in detail and is now recited in the claims for clarification.

Furthermore, Applicants submit that the specification provides sufficient guidance to one of skill in the art to identify and select other proteins having the structural and functional characteristics recited in the claims. Each of the structural domains recited in Claim 1 is well defined and characterized in the art so that it could be readily identified by a skilled person. The specification provides additional description of the domains by reference to the sequence of the exemplary

isolated protein represented by SEQ ID NO:2 or SEQ ID NO:4 and comparison of the domain structures to known sequences (e.g., see pages 40-42). The specification teaches that the domains can be identified by sequence analysis, by homology to the exemplary proteins, or by PCR (e.g., page 5, lines 13-17). Page 4, lines 20-22 teaches that one can use consideration of sequence and structural homology to the exemplary sequences (e.g., SEQ ID NO:2 or SEQ ID NO:4) and can identify or confirm candidate proteins in this manner. Therefore, a first step of selecting candidate proteins having the required structural features as claimed would not require undue experimentation, since the level of skill in the field of molecular and protein biology is high, and since it would be expected that the genus of proteins encompassed by the recited structural characteristics would not be large.

In addition, the protein must meet the functional limitation of a syntaxin-like protein of the invention. As referenced at page 5, lines 16-18, the specification provides working examples demonstrating how one of skill in the art can readily identify whether a protein is an ABA signalling component. As discussed above, assays for detecting whether a protein is capable of affecting ABA-mediated control of ion channels are described in detail in the specification and one of skill in the art would readily be able to test a candidate protein for such activity. For example, one may use *Xenopus laevis* oocytes and confirm the results using guard cells in plants (see pages 19-48 and the Examples). As set forth in these pages, these systems can be used to express candidate proteins in the oocytes and then detect changes in the ABA response, such as by using the voltage clamp experiments described. The role of sequences identified using this method can be confirmed by any one of a number of techniques known in the art including expression pattern analysis, complementation, over-expression, gene knockout, etc. For example, the Examples section also describes the expression of a protein of the invention in a plant to test for the ability of the protein (or an agent that blocks the expression of the protein, such as antisense) to affect the plant's response to stress (e.g., see Example 35).

Therefore, it is submitted that it would not require undue experimentation for one of skill in the art to identify and select proteins meeting the limitations of the claims. In view of the foregoing remarks, Applicants respectfully request that the Examiner withdraw the rejection of Claims 1-3, 13-17, 18, 20 and 26 under 35 U.S.C. § 112, first paragraph.

Objection to the Specification and Rejection of Claims 1-20 and 26 Under 35 U.S.C. § 112, First Paragraph:

The Examiner has objected to the specification and rejected Claims 1-20 and 26 under 35 U.S.C. § 112, first paragraph, on the basis of written description. First, the Examiner contends that the claims lack written description because there is allegedly no correlation of structure and function. The Examiner suggests that functional language be provided in the claims. With regard to Claim 17, the Examiner contends that the specification does not teach a mammalian protein responsive to ABA. With regard to Claims 19 and 20, the Examiner asserts that the specification does not provide any protein which binds to SEQ ID NO:2, for example.

Applicants respectfully traverse the rejection of Claims 1-20 and 26 under 35 U.S.C. § 112, first paragraph. Initially, it is noted that Claim 1 has been amended to more particularly describe the function of the recited protein. In addition, the various fragments and variants of the claimed proteins are now described by a functional characteristic. Support for this amendment has been previously discussed. Claim 1 has also been amended to recite that the protein comprises four and optionally, all five, of the recited structural characteristics. Proteins having a similar domain structures (although not having all four or five together) are known in the art and therefore, one can clearly envision a protein having any of the recited domain structures (e.g., see pages 40-42 and Figures 10 and 41). Moreover, the specification clearly demonstrates the correlation between a protein having these domain structures and the recited activity by the working examples using SEQ ID NO:2. It is submitted that the genus of proteins having the recited structural and functional characteristics is not expected to be highly variable because of the number of structural characteristics required combined with the defined function exhibited by the protein. Therefore, the exemplification and description of the protein that is recited in Claim 1 and related claims provides a clear written description that is sufficient to distinguish it from other proteins and convey to the skilled artisan that Applicants were in possession of such regulators of ABA signalling at the time of the invention.

Similarly, with regard to the added claims which recite proteins having a structural and functional identity to the exemplified sequences, it is submitted that the specification describes how one can measure the sequence homology (page 3, line 1 to page 4, line 5). The procedures that can

be used to make and identify DNAs that fall within the scope of this claim are conventional in the art and an assay is described to identify proteins having the claimed activity (see Examples and previous discussions). There is not substantial variation in the genus because all members must have at least a recited percent homology (identity) to the reference sequence and must have the recited activity. The disclosed species are representative of the genus because all members have at least the recited structural identity with the recited sequence and because of the provision in the specification of assays to identify variants having the recited biological activity.

With regard to Claim 17, it is submitted that mammalian homologues of syntaxin proteins have been identified for other syntaxins (see pages 40-42), and therefore it is expected that a mammalian homologue of the claimed protein can be identified. Moreover, it is well within the ability of one of skill in the art to use the guidance provided in the specification and the high level of skill in the art to screen for proteins that are homologues of the exemplified plant genes. This is discussed, for example, on page 9.

With regard to Claims 19 and 20, Applicants have amended Claim 19 to more particularly describe a method to identify proteins that bind to the proteins identified in the preceding claims. Contrary to the Examiner's contention that the specification does not describe any protein that binds to SEQ ID NO:2, it is noted that the specification teaches at page 6, lines 12-16, that there is interaction between the SYR protein of the present invention and a protein which is identified as having a phosphatase inhibitor domain. Moreover, as discussed in the specification, SEQ ID NO:2 is described as a syntaxin-like protein and syntaxins are known in the art to associate with other proteins (e.g., see page 38, lines 16-27).

In view of the foregoing amendments and remarks, Applicants respectfully request that the Examiner withdraw the rejection of Claims 1-20 and 26 under 35 U.S.C. § 112, first paragraph.

Rejection of Claims 18, 19 and 26 Under 35 U.S.C. § 112, Second Paragraph:

The Examiner has rejected Claims 18, 19 and 26 under 35 U.S.C. § 112, second paragraph, contending that these claims are indefinite. The Examiner contends that Claim 18 refers to a protein comprising the amino acid sequence depicted in SEQ ID NO:3, which is a nucleotide sequence.

Claim 19 is rejected as not setting forth specific method steps. Claim 26 is rejected as depending from a non-elected claim.

Claim 18 has been amended to refer to SEQ ID NO:4 instead of SEQ ID NO:3. Claim 19 has been amended to recite method steps. Support for this amendment was discussed above. Claim 26 has been canceled without prejudice to or disclaimer of the subject matter therein.

In view of the foregoing amendments, Applicants respectfully request that the rejection of Claims 18, 19 and 26 under 35 U.S.C., § 112, second paragraph be withdrawn.

Rejection of Claims 1, 17, 20 and 26 Under 35 U.S.C. § 102(b):

The Examiner has rejected Claims 1, 17, 20 and 26 under 35 U.S.C. § 102(b), contending that these claims are anticipated by Leung et al. The Examiner asserts that Leung et al. teach *Arabidopsis* ABA response gene product ABI1, which is a calcium-modulated protein phosphatase. The Examiner contends that this phosphatase comprises EF hand consensus sequence.

Applicants traverse the rejection of Claims 1, 17, 20 and 26 under 35 U.S.C. § 102(b). Leung et al. disclose a protein that is involved in the ABA response in *Arabidopsis*. The protein comprises an EF-hand flanked on both sides by segments with predicted α-helical conformation. Leung et al. does not teach or suggest the protein recited in Claim 1, as amended, which includes: (i) a hydrophobic C-terminus; (ii) at least one coiled coil region; (iii) an EF-hand consensus sequence; (iv) a nucleotide binding site; and optionally (v) a hydrophilic N-terminus, and which affects ABA signalling as measured by its ability to affect ABA-mediated control of ion channels.

In view of the foregoing remarks, Applicants respectfully request that the Examiner withdraw the rejection of Claims 1, 17, 20 and 26 under 35 U.S.C. § 102(b).

Rejection of Claims 1, 17, 20 and 26 Under 35 U.S.C. § 102(b):

The Examiner has rejected Claims 1, 17, 20 and 26 under 35 U.S.C. § 102(b), contending that these claims are anticipated by Silhavy et al. The Examiner contends that Silhavy et al. teach a stress gene product, DS2, from *S. chacoense* that has a hydrophilic N-terminal region, a coiled coil region, a hydrophobic C-terminal and is weakly responsive to ABA from plants.

Applicants traverse the rejection of Claims 1, 17, 20 and 26 under 35 U.S.C. § 102(b). Silhavy et al. discloses a stress gene DS2 that has a hydrophilic N-terminal region and a hydrophobic C-terminal region. It is thought to include some coil structure. However, Silhavy et al. do not teach or suggest a protein that affects ABA responses as recited in Claim 1, as amended, which includes: (i) a hydrophobic C-terminus; (ii) at least one coiled coil region; (iii) an EF-hand consensus sequence; (iv) a nucleotide binding site; and optionally (v) a hydrophilic N-terminus, and which affects ABA signalling as measured by its ability to affect ABA-mediated control of ion channels. Moreover, Silhavy et al. do not teach that DS2 affects an ABA response. Silhavy et al. investigate the effect of ABA on DS2 expression, but do not investigate whether DS2 affects an ABA response. At best, DS2 appears to be a target of the ABA response rather than a transducer or modulator thereof, and indeed, Silhavy et al. question whether DS2 is responsive to ABA at all (see Discussion in Silhavy et al.). Therefore, there is at best only a tenuous link between DS2 and ABA signalling.

In view of the foregoing remarks, Applicants respectfully request that the Examiner withdraw the rejection of Claims 1, 17, 20 and 26 under 35 U.S.C. § 102(b).

Applicants have attempted to respond to all of the Examiner's concerns as set forth in the November 20 Office Action. The Examiner is encouraged to contact the below-named agent at (303) 863-9700 if there are any questions or concerns regarding Applicants' position.

Respectfully submitted,

SHERIDAN ROSS P.C.

By: Angela Dallas

Angela K. Dallas
Registration No. 42,460
1560 Broadway, Suite 1200
Denver, CO 80202-5141
(303) 863-9700

Date: February 20, 2003

In the Specification:

On page 1, line 1, immediately following the title, please insert the following new paragraph:

--This application claims the benefit of priority under 35 U.S.C. § 371 to PCT Patent Application No. PCT/GB98/02937, filed September 30, 1998, which designated the United States and was published in English, and which claims the benefit of foreign priority under 35 U.S.C. § 119 to Great Britain Patent Application No. 9720784.9, filed September 30, 1997.--

On page 2, please replace the paragraph spanning lines 20-21 with the following paragraph:

--The features of the protein can be defined as follows with reference to [SEQ. ID No. 2]SEQ ID NO:2.--

On page 2, please replace the paragraph spanning lines 29-30 with the following paragraph:

--In an especially preferred embodiment, the protein comprises the amino acid sequence shown in [SEQ ID No. 2]SEQ ID NO:2 or [SEQ ID No 4]SEQ ID NO:4.--

On page 3, please replace the paragraph spanning lines 1-5 with the following paragraph:

--The present invention includes variants of the protein defined above. Such variants include proteins having 50% or more overall homology with the sequence of [Seq ID No. 2]SEQ ID NO:2. Typically the homology is 60% or more, more typically 65%, preferably 70%, more preferably 75%, even more preferably 80% or 85%, especially preferred are 90%, 95%, 98% or 99% homology.--

On page 3, please replace the paragraph spanning lines 6-12 with the following paragraph:

--Percentage homology preferably is calculated on the basis of amino acids that are identical in corresponding positions in the two sequences under consideration. Conservative substitutions are not taken into account. In calculation of percentage homology of a putative protein under investigation with the [SEQ ID No. 2]SEQ ID NO:2 or SEQ ID NO:4, if the protein under investigation has a different length, then the calculation is based on the amino acids in the portion of the molecule under investigation that overlaps with the sequence shown in [Seq ID No. 2]SEQ ID NO:2 or SEQ ID NO:4.--

On page 3, please replace the paragraph spanning lines 21-27 with the following paragraph:

--Sequence homology (or identity) may moreover be determined using any suitable homology algorithm, using for example default parameters. Advantageously, the BLAST algorithm is employed, with parameters set to default values. The BLAST algorithm is described in detail [at http://www.ncbi.nih.gov/BLAST/blast_help.html] in, for example: Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Madden, T.L., Tatusov, R.L. & Zhang, J. (1996) "Applications of network BLAST server" Meth. Enzymol. 266:131-141. ; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272; Altschul, S.F., Madden, T.L., Schääffer, A.A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D.J. (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs." Nucleic Acids Res. 25:3389-3402; Karlin, S. & Altschul, S.F. (1990) "Methods for assessing the statistical significance of molecular sequence features by using general scoring schemes." Proc. Natl. Acad. Sci. USA 87:2264-2268; Karlin, S. & Altschul, S.F. (1993) "Applications and statistics for multiple high-scoring segments in molecular sequences." Proc. Natl. Acad. Sci. USA 90:5873-5877, which [is]are incorporated herein by reference. The search parameters are defined as follows, and are advantageously set to the defined default parameters.--

On page 5, please replace the paragraph spanning lines 8-18 with the following paragraph:

--Although in the specific non-limiting example described below the ABA signalling component was obtained from *Nicotiana tabacumm* (tobacco) the present invention relates in general to an ABA signalling component. For example, ABA signalling components from dicotyledonous and monocotyledonous plants, including cereals such as wheat, barley, rice, maize and sorghum; field crops other than tobacco such as canola, sunflower, sugarbeet and cotton; fruit and vegetables. As an example, the corresponding ABA signalling component in maize may be found using reverse transcription followed by polymerase chain reaction (RT-PCR) using known techniques and primers devised from the sequences of [Seq ID No. 1]SEQ ID NO:1. Confirmation that an ABA signalling component has been arrived at can be achieved using the assays of the present invention and described herein.--

On page 5, please replace the paragraph spanning lines 19-22 with the following paragraph:

--Using this approach we have also determined the corresponding ABA signalling component from *Arabidopsis thaliana*. The nucleic acid sequence is shown as [Seq ID No. 3]SEQ ID NO:3 and corresponding amino acid sequence as [Seq ID No. 4]SEQ ID NO:4. The present invention also includes variants of these sequences as defined herein.--

On page 6, please replace the paragraph spanning lines 17-25 with the following paragraph:

--Also included within the present invention are truncated proteins derivable from the proteins defined above. Typically such truncated proteins will be able to compete with the non-truncated protein in an ABA signalling pathway, and/or be capable of giving rise to antibodies to the non-truncated protein. Examples of such truncated proteins include Sp1 comprising amino acids 115-127 of [SEQ. ID No. 2]SEQ ID NO:2 and Sp2 comprising amino acids 1-279 of [SEQ. ID No. 2]SEQ ID NO:2. Thus, the present invention further includes a method of raising immunoglobins comprising administering a protein of the present invention to a mammal, such as a rabbit or human, and optionally isolating the immunoglobins generated.--

On page 6, please replace the paragraph spanning lines 28-30 with the following paragraph:

--In particular, according to another aspect of the present invention there is provided nucleic acid comprising the sequence from positions 18 to 917 shown in [SEQ. ID No. 1]SEQ ID NO:1, or from positions 77 to 991 shown in [SEQ. ID No. 3]SEQ ID NO:3.--

On page 17, please replace the paragraph spanning lines 21-22 with the following paragraph:

--Figure 40 (or [SEQ. ID No. 5]SEQ ID NO:5) shows the antisense cDNA SYR cloned into pG3SA;--

On page 78, please replace the paragraph spanning lines 10-12 with the following paragraph:

--Sequence homology searches were performed at the BLAST sequence similarity service, provided by NCBI (National Centre for Biotechnology Information, [http://www.ncbi.nlm.nih.gov/]described in detail previously herein).--

On page 111, please replace the paragraph spanning lines 7-20 with the following paragraph:

--Originally three leaves of three different plants were infiltrated with pGSA, the construct containing the antisense cDNA of *syr* (Fig. 40; [SEQ ID No. 3]SEQ ID NO:3) under the control of the 35S promoter. After three days of incubation at 23 C and 100% humidity, the plants were tested for different wilty phenotype in the leaves. The plants with soil were transferred from their 100%

humidity environment to a dry place 30 cm under 180 W lamps. The leaves transformed with the pGSA seem to start wilting sooner than the control non-infiltrated leaves. This means that after approximately 5 min, the tip and edges (where the pGSA was infiltrated) of the transformed leaf were starting to hang down and being wilty, whereas the other leaves only started to dry out at approximately 10 min after the transfer. This was recorded for two of the three plants. The two transformed leaves were tested for GUS activity. Blue stains as result of the GUS activity were detected in approximately 10% of the cells in the infiltrated area, indicating gene expression via the 35S promoter was occurring in the plant cells. No GUS activity was detected in two control leaves tested.--

In the Claims:

Claims 3, 21-56 have been canceled.

Claims 1, 2 and 4-20 have been amended as shown below.

Claims 57-65 have been added.

1. (Once Amended) [A] An isolated protein capable of affecting an ABA response and comprising[one or more of the following]:

(i) a hydrophobic C-terminus;

(ii) at least one coiled coil region;

(iii) an EF-hand consensus sequence;

(iv) a nucleotide binding site; and optionally

(v) a hydrophilic N-terminus;

or a biologically active fragment or variant thereof;

wherein said protein, fragment or variant thereof affects ABA signalling as measured by its ability to affect ABA-mediated control of ion channels.

2. (Once Amended) [A] An isolated protein according to claim 1 which is capable of being cleaved by the toxin botulinum C.

4. (Twice Amended) [A] An isolated protein according to Claim 1 wherein the hydrophobic C-terminus comprises the sequence from position 282 to position 296 of the amino acid sequence shown in [SEQ ID No. 2]SEQ ID NO:2 .

5. (Once Amended) [A] An isolated protein according to claim 4 wherein the hydrophobic C-terminus comprises the sequence from position 280 to position 294 of the amino acid sequence shown in [SEQ ID No. 2]SEQ ID NO:2.

6. (Twice Amended) [A] An isolated protein according to Claim 1 wherein said at least one coiled coil [regions] region comprises the sequence from position 210 to position 247 of the amino acid[-] sequence shown in [SEQ ID No 2]SEQ ID NO:2.

7. (Twice Amended) [A] An isolated protein according to Claim 6 wherein said at least one coiled coil regions comprises the sequence from position 216 to position 240 of the amino acid sequence shown in [SEQ ID No 2]SEQ ID NO:2.

8. (Twice Amended) [A] An isolated protein according to Claim 1 wherein said hydrophilic N-terminus comprises the sequence from position 1 to position 280 of the amino acid sequence shown in [SEQ ID No 2]SEQ ID NO:2.

9. (Once Amended) [A] An isolated protein according to claim 8 wherein the hydrophilic N-terminus comprises the sequence from position 1 to position 279 of the amino acid sequence shown in [SEQ ID No 2]SEQ ID NO:2.

10. (Twice Amended) [A] An isolated protein according to Claim 1 wherein said nucleotide binding site comprises the sequence of positions 114 to 119 of the amino acid sequence shown in [SEQ ID No 2]SEQ ID NO:2.

11. (Twice Amended) [A] An isolated protein according to Claim 1 wherein the nucleotide binding site comprises the sequence of positions 116, 118 and 120 of the amino acid sequence shown in [SEQ ID No 2]SEQ ID NO:2.

12. (Twice Amended) [A] An isolated protein according to Claim 1 wherein said EF-hand consensus sequence comprises the sequence from position 16 to 28 of the amino acid sequence shown in [SEQ ID No. 2]SEQ ID NO:2.

13. (Twice Amended) [A] An isolated protein according to Claim 1 wherein said hydrophobic C-terminus comprises a membrane spanning region.

14. (Twice Amended) [A] An isolated protein according to Claim 1 wherein there are three coiled coil regions.

15. (Twice Amended) [A] An isolated protein according to Claim 1 wherein said at least one coiled coil region corresponds to an epimorphin pattern.

16. (Twice Amended) [A] An isolated protein according to Claim 6 wherein said at least one coiled coil region corresponds to an epimorphin pattern.

17. (Twice Amended) [A] An isolated protein according to Claim 1 that is derived from a plant[,] or a mammal.

18. (Once Amended) [A] An isolated protein comprising the amino acid sequence shown in [Seq ID No. 2]SEQ ID NO:2 or [3]SEQ ID NO:4, or a biologically active fragment or variant thereof, wherein said protein, fragment thereof or variant thereof affects ABA signalling as measured by its ability to affect ABA-mediated control of ion channels.

19. (Twice Amended) [A] An isolated method of screening for protein-protein interaction comprising:

a) contacting a protein according to any one of Claims 1-18 with an expressed candidate ABA signalling component; and

b) detecting interaction between said protein and said ABA signalling component[the use of a protein of Claim 1 and selecting compounds exhibiting said interaction].

20. (Once Amended) [A] An isolated protein selected using the method of claim 19.